

## Alignments

>emb|V00866.1|HBVADW Hepatitis B virus complete DNA sequence (subtype adw)  
Length=3200

Score = 5906 bits (3198), Expect = 0.0  
Identities = 3198/3198 (100%), Gaps = 0/3198 (0%)  
Strand=Plus/Plus

Query 3	TTCACACTGCTTGACCAAGCTCTGCAGGGATCCCAAGAGTCAGGGGTCTGTATCTTCTGC	62
Sbjct 1	TCACACTGCTTGACCAAGCTCTGCAGGGATCCCAAGAGTCAGGGGTCTGTATCTTCTGC	60
Query 63	TGGTGGCTCCAGTTCAAGAACAGTAACCCCTGCTCCGAATATTGCCCTCACATCTCGTC	122
Sbjct 61	GGTGGCTCCAGTTCAAGAACAGTAACCCCTGCTCCGAATATTGCCCTCACATCTCGTC	120
Query 123	AATCTCCGGGAGGACTGGGACCCCTGTGACGATCATGGGAAACATCACATCAGGATTCT	182
Sbjct 121	ATCTCCGGGAGGACTGGGACCCCTGTGACGATCATGGGAAACATCACATCAGGATTCT	180
Query 183	AGGACCCCTGCTCGTGTACAGGGGGGTTTTCTTGTGACAAGAACTCTCACAAATACC	242
Sbjct 181	GGACCCCTGCTCGTGTACAGGGGGTTTTCTTGTGACAAGAACTCTCACAAATACC	240
Query 243	GCAGAGTCTAGACTCGTGGGACTCTCTCAATTCTAGGGGATCACCCGTGTGCT	302
Sbjct 241	CAGAGTCTAGACTCGTGGGACTCTCTCAATTCTAGGGGATCACCCGTGTGCT	300
Query 303	TGGCCAAAATTCGCACTCCCAACCTCCAATCACTCACCAACCTCTGCTCTCCAATTG	362
Sbjct 301	GGCCAAAATTCGCACTCCCAACCTCCAATCACTCACCAACCTCTGCTCTCCAATTG	360
Query 363	TCCCTGGTTATCGCTGGATGTGTCTGGCGCTTTTATCATATTCTCTCATCTCTGCTGCT	422
Sbjct 361	CCCTGGTTATCGCTGGATGTGTCTGGCGCTTTTATCATATTCTCTCATCTCTGCTGCT	420
Query 423	ATGCCCTCATCTTATTGGTTCTCTGGATTACAAGGTATGTTGCCGTTGTCTCT	482
Sbjct 421	TGCCCTCATCTTATTGGTTCTCTGGATTACAAGGTATGTTGCCGTTGTCTCT	480
Query 483	AATTCAGGATCAACAAACACCAGTACGGGACCATGCAAAACCTGCACGACTCTGCTCA	542
Sbjct 481	ATTCAGGATCAACAAACACCAGTACGGGACCATGCAAAACCTGCACGACTCTGCTCA	540
Query 543	AGGCCAACTCTAAGTTCCCTCATGTTGTCGACAAAACCTACGGATGGAATTGCACTG	602
Sbjct 541	GGCCAACTCTAAGTTCCCTCATGTTGTCGACAAAACCTACGGATGGAATTGCACTG	600
Query 603	TATTCGCATCCCCTGCTGGGTTTCGCaaaATACCTATGGGATGGGGCTCAGTCAG	662
Sbjct 601	ATTCGCATCCCCTGCTGGGTTTCGCaaaATACCTATGGGATGGGGCTCAGTCAG	660
Query 663	TTTCCTTGCTCAGTTACTAGTGCCTTGTGTCAGTGGTTCTGAGGGCTTCCCCCAC	722
Sbjct 661	TTTCCTTGCTCAGTTACTAGTGCCTTGTGTCAGTGGTTCTGAGGGCTTCCCCCAC	720
Query 723	TGTTGGCTTCAGCTATAATGGATGATGTTGATTGGGGCCAAGTCTGTACAGCATCGT	782
Sbjct 721	GTTGGCTTCAGCTATAATGGATGATGTTGATTGGGGCCAAGTCTGTACAGCATCGT	780
Query 783	GAGTCCTTATACCGCTGTTACCAATTCTTTGCTCTGGGTATACATTTAACCT	842
Sbjct 781	AGTCCTTATACCGCTGTTACCAATTCTTTGCTCTGGGTATACATTTAACCT	840
Query 843	AACAAAACAAAAAGATGGGTTATCCCTAAACTCTACGGGCTACATAATTGGAAAGTGG	902
Sbjct 841	AACAAAACAAAAAGATGGGTTATCCCTAAACTCTACGGGCTACATAATTGGAAAGTGG	900
Query 903	GGAACTTGGCCACAGGATCATATTGCAAAAGATCACAAACACTGTTTAGAAAACCT	962
Sbjct 901	GAACTTGGCCACAGGATCATATTGCAAAAGATCACAAACACTGTTTAGAAAACCT	960
Query 963	GTAAACAGGCCTATGATGGAAAGTATGTCaaaAGATGGGGTCTTTGGGCTTGT	1022
Sbjct 961	TTAACAGGCCTATGATGGAAAGTATGTCaaaAGATGGGGTCTTTGGGCTTGT	1020
Query 1023	GCTCCATTACACAAATGTTGATCTCGCTTAATGCCCTTGTATGCAATGATAACAGCT	1082
Sbjct 1021	CTCCATTACACAAATGTTGATCTCGCTTAATGCCCTTGTATGCAATGATAACAGCT	1080

Query	1083	AAACAGGGCTTCACTTTCTGCCAACCTTACAAGGCCCTTCTAAGTAAACAGTACATGAAC	1142
Sbjct	1081	AAACAGGGCTTCACTTTCTGCCAACCTTACAAGGCCCTTCTAAGTAAACAGTACATGAAC	1140
Query	1143	CTTACCCCGTTGCTCGCAACGCCCTGGCTGTGCCAAGTGTGCTGCGAACCCCC	1202
Sbjct	1141	CTTACCCCGTTGCTCGCAACGCCCTGGCTGTGCCAAGTGTGCTGCGAACCCCC	1200
Query	1203	ACTGGCTGGGGCTAGGCCATAGGCCATCAGCGCATGGCTGAAACCTTGTGGCTCCCTG	1262
Sbjct	1201	ACTGGCTGGGGCTAGGCCATAGGCCATCAGCGCATGGCTGAAACCTTGTGGCTCCCTG	1260
Query	1263	CCGATCCATACTGGAAACTCTAGGCCCTGGCTGTTTGCTCGCAGCGGCTGGAGCAAAG	1322
Sbjct	1261	CCGATCCATACTGGAAACTCTAGGCCCTGGCTGTTTGCTCGCAGCGGCTGGAGCAAAG	1320
Query	1323	CTCATCGGAACGTGACAATCTGTGTCCTCTCGCGGAAATAACATCATATTCCATGGCTG	1382
Sbjct	1321	CTCATCGGAACGTGACAATCTGTGTCCTCTCGCGGAAATAACATCATATTCCATGGCTG	1380
Query	1383	CTAGGCTGTACTGCCAATGGATCTTGCAGGGGACGTCTTGTGTTACGTCCCCTGGCG	1442
Sbjct	1381	CTAGGCTGTACTGCCAATGGATCTTGCAGGGGACGTCTTGTGTTACGTCCCCTGGCG	1440
Query	1443	CTGAATCCCGCGGACGACCCCTCTGGGGCGCTTGGGACTCTCTCGTCCCCCTCTCGT	1502
Sbjct	1441	CTGAATCCCGCGGACGACCCCTCTGGGGCGCTTGGGACTCTCTCGTCCCCCTCTCGT	1500
Query	1503	CTGCGGTTCCAGGCCAACCGGGCGCACCTCTTACCGGCTCTCCCGCTGTGCGCT	1562
Sbjct	1501	CTGCGGTTCCAGGCCAACCGGGCGCACCTCTTACCGGCTCTCCCGCTGTGCGCT	1560
Query	1563	TCTCATCGCCGTCGGTGTGCACTTGCCTCACCTCTGACGGTGTGCAATGGGACACCG	1622
Sbjct	1561	TCTCATCGCCGTCGGTGTGCACTTGCCTCACCTCTGACGGTGTGCAATGGGACACCG	1620
Query	1623	TGAACGCCCATCAGATCTGCCAACGGTCTTACATAAGGACTCTTGGACTCCAGCAA	1682
Sbjct	1621	TGAACGCCCATCAGATCTGCCAACGGTCTTACATAAGGACTCTTGGACTCCAGCAA	1680
Query	1683	TGTCAACGACCGACTTGGGCCACTTCAAAGACTGTGTGTTAAGGACTGGGAGGAGT	1742
Sbjct	1681	TGTCAACGACCGACTTGGGCCACTTCAAAGACTGTGTGTTAAGGACTGGGAGGAGT	1740
Query	1743	TGGGGAGGAGATTAGGTTAATGATCTTGTATTAGGAGGCTGTAGGCATAAAATGGCT	1802
Sbjct	1741	TGGGGAGGAGATTAGGTTAATGATCTTGTATTAGGAGGCTGTAGGCATAAAATGGCT	1800
Query	1803	GCGCACCAAGCACCATGCAACTTTTCACTCTGCCATTCTCTTGACATGTCCCCAC	1862
Sbjct	1801	GCGCACCAAGCACCATGCAACTTTTCACTCTGCCATTCTCTTGACATGTCCCCAC	1860
Query	1863	TGTCAAGCTCCAAGCTGCGCTGGGCTTGGGATGGACATTGACCTTATAA	1922
Sbjct	1861	TGTCAAGCTCCAAGCTGCGCTGGGCTTGGGATGGACATTGACCTTATAA	1920
Query	1923	AGAATTGGAGACTGTGGAGTTACTCTGTTTGCCTCTGACTCTTCTCGT	1982
Sbjct	1921	AGAATTGGAGACTGTGGAGTTACTCTGTTTGCCTCTGACTCTTCTCGT	1980
Query	1983	ACGAGATCTCTAGAACCGCCTAGCTGTATCGAGAACGCTTAGAGCTCTGAGCA	2042
Sbjct	1981	ACGAGATCTCTAGAACCGCCTAGCTGTATCGAGAACGCTTAGAGCTCTGAGCA	2040
Query	2043	TTGCTACCTCACCATACTGCACTCAGGCAAGCCATTCTGCTGGGGAAATTGATGAC	2102
Sbjct	2041	TTGCTACCTCACCATACTGCACTCAGGCAAGCCATTCTGCTGGGGAAATTGATGAC	2100
Query	2103	TCTAGCTACCTGGGGTAAATGCAAGATCCAGCATCCAGAGACTAGTAGTC	2162
Sbjct	2101	TCTAGCTACCTGGGGTAAATGCAAGATCCAGCATCCAGAGACTAGTAGTC	2160
Query	2163	TTATGTTAATACATGGGTTAAAGATCAGGCAACTTGTGTTTCATATACTTG	2222
Sbjct	2161	TTATGTTAATACATGGGTTAAAGATCAGGCAACTTGTGTTTCATATACTTG	2220
Query	2223	CCTACTTTGGAAAGAGAGACTGTGACTTGAATTTGGCTCTTGGAGTGTGGATTG	2282
Sbjct	2221	CCTACTTTGGAAAGAGAGACTGTGACTTGAATTTGGCTCTTGGAGTGTGGATTG	2280
Query	2283	CACTCCCTCAGCCTATAGACCAACAAATGCCCTATCTTACAAACACTCCGGAAACTAC	2342

Sbjct	2281	CACTCCTCCAGCTATAGACCACCAAATGCCCTATCTTACACACTCCGGAAACTAC	2340
Query	2343	TGTGTTAGACGACGGGACCGAGGCAGGTCCTAGAAGAAGAACCTCCCTCGCTCGCAG	2402
Sbjct	2341	TGTGTTAGACGACGGGACCGAGGTCCTAGAAGAAGAACCTCCCTCGCTCGCAG	2400
Query	2403	ACCGAGATCTCAATCGCCGCGTCGAGAAGATCTCAATCTCGGAATCTCAATGTTAGTA	2462
Sbjct	2401	ACCGAGATCTCAATCGCCGCGTCGAGAAGATCTCAATCTCGGAATCTCAATGTTAGTA	2460
Query	2463	TTCTTGGACTCATAAAGTGGAAACTTACGGGCTTATTCTCTACAGTACCTATCT	2522
Sbjct	2461	TTCTTGGACTCATAAAGTGGAAACTTACGGGCTTATTCTCTACAGTACCTATCT	2520
Query	2523	TTAACCTGAATGGCAAACCTCTCTTCTTAAGATTCATTACAAGAGGACATTATA	2582
Sbjct	2521	TTAACCTGAATGGCAAACCTCTCTTCTTAAGATTCATTACAAGAGGACATTATA	2580
Query	2583	ATAGGTGCAACAAATTGTGGGCCCTCTACTGTAAATGAAAAGAGAAGATTGAAATTAA	2642
Sbjct	2581	ATAGGTGCAACAAATTGTGGGCCCTCTACTGTAAATGAAAAGAGAAGATTGAAATTAA	2640
Query	2643	TTATGCCCTGCTAGATCTATCTACCCACACTAAATATTGCCCTAGACAAAGGAATTAA	2702
Sbjct	2641	TTATGCCCTGCTAGATCTATCTACCCACACTAAATATTGCCCTAGACAAAGGAATTAA	2700
Query	2703	AACCTTATTATCCAGATCAGGTAGTAACTCATTAACCTCCAAACGACATTATTCATA	2762
Sbjct	2701	AACCTTATTATCCAGATCAGGTAGTAACTCATTAACCTCCAAACGACATTATTCATA	2760
Query	2763	CTCTTGGAAAGGCTGGTATTCTATATAAGAGGGAAACACACGCTAGCGCATCATTTGGG	2822
Sbjct	2761	CTCTTGGAAAGGCTGGTATTCTATATAAGAGGGAAACACACGCTAGCGCATCATTTGGG	2820
Query	2823	GGT CACCA TATTCTGGGAACAAGGGTACAGCAT TCC AAAGGCTGGGACGGAACTT	2882
Sbjct	2821	GGT CACCA TATTCTGGGAACAAGGGTACAGCAT TCC AAAGGCTGGGACGGAACTT	2880
Query	2883	TCGTGTCACCCACCTCTGGGATTCTCCCGATCATCAGTTGGACCCCTGCATTGGAGCC	2942
Sbjct	2881	TCGTGTCACCCACCTCTGGGATTCTCCCGATCATCAGTTGGACCCCTGCATTGGAGCC	2940
Query	2943	AACTCAACAAATCCAGATTGGGACTTCACCCCATCAAGGACCACTGGCCAGCAGCCAAC	3002
Sbjct	2941	AACTCAACAAATCCAGATTGGGACTTCACCCCATCAAGGACCACTGGCCAGCAGCCAAC	3000
Query	3003	CAGGTAGGAGTGGGAGCATTCGGCCAGGGCTCACCCCTCACACGGGGTATTGGGG	3062
Sbjct	3001	CAGGTAGGAGTGGGAGCATTCGGCCAGGGCTCACCCCTCACACGGGGTATTGGGG	3060
Query	3063	TGGAGCCCTCAGGCTAGGGCATATGACCAAGTGTCAACAAATTCTCTCTGCCICC	3122
Sbjct	3061	TGGAGCCCTCAGGCTAGGGCATATGACCAAGTGTCAACAAATTCTCTCTGCCICC	3120
Query	3123	ACCAATCGGCAGTCAGGAAGGCAGCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT	3182
Sbjct	3121	ACCAATCGGCAGTCAGGAAGGCAGCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT	3180
Query	3183	CCTCAGGCCATGCAGTGG 3200	
Sbjct	3181	CCTCAGGCCATGCAGTGG 3198	